

SEQUENCE LISTING

<110> Kinch, Michael S.

<120> EphA2 VACCINES

<130> 10271-148

<150> US 60/532,696

<151> 2003-12-24

<150> US 60/602,588

<151> 2004-08-18

<150>

<151> 2004-10-01

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<170> PatentIn version 3.2

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170

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala

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ctg ctg tgg tgc tgc ctg gcc gcg gcg gcg cag ggc aag

218

Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala Ala Ala Gln Gly Lys

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gaa gtg gta ctg ctg gac ttt gct gca gct gga ggg gag ctc ggc tgg

266

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314

Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met

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aat gac atg ccg atc tac atg tac tcc gtg tgc aac gtg atg tct ggc

362

Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly

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gac cag gac aac tgg ctc cgc acc aac tgg gtg tac cga gga gag gct

410

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80	85	90	
gag cgt atc ttc att gag ctc aag ttt act gta cgt gac tgc aac agc Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser 95	100	105	458
ttc cct ggt ggc gcc agc tcc tgc aag gag act ttc aac ctc tac tat Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr 110	115	120	506
gcc gag tcg gac ctg gac tac ggc acc aac ttc cag aag cgc ctg ttc Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe 125	130	135	554
acc aag att gac acc att gcg ccc gat gag atc acc gtc agc agc gac Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp 140	145	150	602
ttc gag gca cgc cac gtg aag ctg aac gtg gag gag cgc tcc gtg ggg Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly 160	165	170	650
ccg ctc acc cgc aaa ggc ttc tac ctg gcc ttc cag gat atc ggt gcc Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala 175	180	185	698
tgt gtg gcg ctg ctc tcc gtc cgt gtc tac tac aag aag tgc ccc gag Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu 190	195	200	746
ctg ctg cag ggc ctg gcc cac ttc cct gag acc atc gcc ggc tct gat Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp 205	210	215	794
gca cct tcc ctg gcc act gtg gcc ggc acc tgt gtg gac cat gcc gtg Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala Val 220	225	230	842
gtg cca ccc ggg ggt gaa gag ccc cgt atg cac tgt gca gtg gat ggc Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp Gly 240	245	250	890
gag tgg ctg gtg ccc att ggg cag tgc ctg tgc cag gca ggc tac gag Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu 255	260	265	938
aag gtg gag gat gcc tgc cag gcc tgc tcg cct gga ttt ttt aag ttt Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe 270	275	280	986
gag gca tct gag agc ccc tgc ttg gag tgc cct gag cac acg ctg cca Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro 285	290	295	1034
tcc cct gag ggt gcc acc tcc tgc gag tgt gag gaa ggc ttc ttc cgg Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Pro Glu His Phe Phe Arg 300	305	310	1082
gca cct cag gac cca gcg tcg atg cct tgc aca cga ccc ccc tcc gcc Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala 320	325	330	1130

cca cac tac ctc aca gcc gtg ggc atg ggt gcc aag gtg gag ctg cgc	1178
Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg	
335 340 345	
tgg acg ccc cct cag gac agc ggg ggc cgc gag gac att gtc tac agc	1226
Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser	
350 355 360	
gtc acc tgc gaa cag tgc tgg ccc gag tct ggg gaa tgc ggg ccg tgt	1274
Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys	
365 370 375	
gag gcc agt gtg cgc tac tcg gag cct cct cac gga ctg acc cgc acc	1322
Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr	
380 385 390 395	
agt gtg aca gtg agc gac ctg gag ccc cac atg aac tac acc ttc acc	1370
Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr	
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gtg gag gcc cgc aat ggc gtc tca ggc ctg gta acc agc cgc agc ttc	1418
Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe	
415 420 425	
cgt act gcc agt gtc agc atc aac cag aca gag ccc ccc aag gtg agg	1466
Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg	
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Leu Glu Gly Arg Ser Thr Ser Leu Ser Val Ser Trp Ser Ile Pro	
445 450 455	
ccg ccg cag cag agc cga gtg tgg aag tac gag gtc act tac cgc aag	1562
Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys	
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Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser	
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Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val	
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cag gca ctg acg cag gag ggc cag ggg gcc ggc agc aag gtg cac gaa	1706
Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu	
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Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly	
525 530 535	
ggc gtg gct gtc ggt gtg gtc ctg ctt ctg gtg ctg gca gga gtt ggc	1802
Gly Val Ala Val Gly Val Val Leu Leu Val Leu Ala Gly Val Gly	
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Phe Phe Ile His Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro	
560 565 570	

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Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr				
tac gtg gac ccc cac aca tat gag gac ccc aac cag gct gtg ttg aag	590	595	600	1946
Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys				
ttc act acc gag atc cat cca tcc tgt gtc act cgg cag aag gtg atc	605	610	615	1994
Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys Val Ile				
gga gca gga gag ttt ggg gag gtg tac aag ggc atg ctg aag aca tcc	620	625	630	2042
Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser				
tcg ggg aag aag gag gtg ccg gtg gcc atc aag acg ctg aaa gcc ggc	640	645	650	2090
Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly				
tac aca gag aag cag cga gtg gac ttc ctc ggc gag gcc ggc atc atg	655	660	665	2138
Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met				
ggc cag ttc agc cac aac atc atc cgc cta gag ggc gtc atc tcc	670	675	680	2186
Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser				
aaa tac aag ccc atg atg atc act gag tac atg gag aat ggg gcc	685	690	695	2234
Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala				
ctg gac aag ttc ctt cgg gag aag gat ggc gag ttc agc gtg ctg cag	700	705	710	2282
Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln				
ctg gtg ggc atg ctg cgg ggc atc gca gct ggc atg aag tac ctg gcc	720	725	730	2330
Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala				
aac atg aac tat gtg cac cgt gac ctg gct gcc cgc aac atc ctc gtc	735	740	745	2378
Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val				
aac agc aac ctg gtc tgc aag gtg tct gac ttt ggc ctg tcc cgc gtg	750	755	760	2426
Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val				
ctg gag gac gac ccc gag gcc acc tac acc acc agt ggc ggc aag atc	765	770	775	2474
Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Ser Gly Gly Lys Ile				
ccc atc cgc tgg acc gcc cgg gag gcc att tcc tac cgg aag ttc acc	780	785	790	2522
Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr				
tct gcc agc gac gtg tgg agc ttt ggc att gtc atg tgg gag gtg atg	800	805	810	2570
Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu Val Met				
acc tat ggc gag cgg ccc tac tgg gag ttg tcc aac cac gag gtg atg				2618

Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met			
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aaa gcc atc aat gat ggc ttc cgg ctc ccc aca ccc atg gac tgc ccc		2666	
Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro			
830	835	840	
tcc gcc atc tac cag ctc atg atg cag tgc tgg cag cag gag cgt gcc		2714	
Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala			
845	850	855	
cgc cgc ccc aag ttc gct gac atc gtc agc atc ctg gac aag ctc att		2762	
Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile			
860	865	870	875
cgt gcc cct gac tcc ctc aag acc ctg gct gac ttt gac ccc cgc gtg		2810	
Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val			
880	885	890	
tct atc cgg ctc ccc agc acg agc ggc tcg gag ggg gtg ccc ttc cgc		2858	
Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg			
895	900	905	
acg gtg tcc gag tgg ctg gag tcc atc aag atg cag cag tat acg gag		2906	
Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu			
910	915	920	
cac ttc atg gcg gcc ggc tac act gcc atc gag aag gtg gtg cag atg		2954	
His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met			
925	930	935	
acc aac gac gac atc aag agg att ggg gtg cgg ctg ccc ggc cac cag		3002	
Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln			
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aag cgc atc gcc tac agc ctg ctg gga ctc aag gac cag gtg aac act		3050	
Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr			
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gtg ggg atc ccc atc tga gcctcgacag ggcctggagc cccatcgccc		3098	
Val Gly Ile Pro Ile			
975			
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20							25								

Asp	Phe	Ala	Ala	Ala	Gly	Gly	Glu	Leu	Gly	Trp	Leu	Thr	His	Pro	Tyr
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Gly	Lys	Gly	Trp	Asp	Leu	Met	Gln	Asn	Ile	Met	Asn	Asp	Met	Pro	Ile
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Tyr	Met	Tyr	Ser	Val	Cys	Asn	Val	Met	Ser	Gly	Asp	Gln	Asp	Asn	Trp
65					70										80

Leu	Arg	Thr	Asn	Trp	Val	Tyr	Arg	Gly	Glu	Ala	Glu	Arg	Ile	Phe	Ile
85															95

Glu	Leu	Lys	Phe	Thr	Val	Arg	Asp	Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala
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Ser	Ser	Cys	Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu
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Asp	Tyr	Gly	Thr	Asn	Phe	Gln	Lys	Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr
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Ile	Ala	Pro	Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp	Phe	Glu	Ala	Arg	His
145					150										160

Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys

165

170

175

Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu
 180 185 190

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu
 195 200 205

Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala
 210 215 220

Thr Val Ala Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly
 225 230 235 240

Glu Glu Pro Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro
 245 250 255

Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala
 260 265 270

Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser
 275 280 285

Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala
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Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro
 305 310 315 320

Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr
 325 330 335

Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln
 340 345 350

Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln
 355 360 365

Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg
 370 375 380

Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser
 385 390 395 400

Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn
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Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val
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Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser
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Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser
450 455 460

Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn
465 470 475 480

Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp
485 490 495

Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln
500 505 510

Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu Phe Gln Thr Leu Ser
515 520 525

Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly
530 535 540

Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg
545 550 555 560

Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe
565 570 575

Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His
580 585 590

Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
595 600 605

His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
610 615 620

Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
625 630 635 640

Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln
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Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His
660 665 670

His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
675 680 685

Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu
690 695 700

Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu
705 710 715 720

Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
725 730 735

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
740 745 750

Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
755 760 765

Glu Ala Thr Tyr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
770 775 780

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
785 790 795 800

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
805 810 815

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
820 825 830

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
835 840 845

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
850 855 860

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
865 870 875 880

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
885 890 895

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
900 905 910

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
915 920 925

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
930 935 940

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
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 gagccccgta tgcactgtgc agtggatggc gagtggctgg tgcccatgg gcagtgcctg 960
 tgccaggcag gctacgagaa ggtggaggat gcctgccagg cctgctcgcc tggattttt 1020
 aagtttggagg catctgagag cccctgcttgc gactgcccctg agcacacgct gccatcccc 1080

gagggtgcca cctcctgcga gtgtgaggaa ggcttcttcc gggcacctca ggacccagcg	1140
tcgatgcctt gcacacgacc cccctccgcc ccacactacc tcacagccgt gggcatgggt	1200
gccaaagggtgg agctgcgctg gacgccccct caggacagcg ggggcccgcga ggacattgtc	1260
tacagcgtca cctgcgaaca gtgctggcc gagtctgggg aatgcgggccc gtgtgaggcc	1320
agtgtgcgct actcggagcc tcctcacgga ctgacccgca ccagtgtgac agtgagcgcac	1380
ctggagcccc acatgaacta caccttacc gtggaggccc gcaatggcgt ctcaggcctg	1440
gtaaccagcc gcagcttccg tactgccagt gtcagcatca accagacaga gccccccaag	1500
gtgaggctgg agggccgcag caccacctcg cttagcgtct cctggagcat ccccccgcg	1560
cagcagagcc gagtgtggaa gtacgaggtc acttaccgca agaagggaga ctccaacagc	1620
tacaatgtgc gcccgcaccga gggtttctcc gtgaccctgg acgacccgtc cccagacacc	1680
acctacctgg tccaggtgca ggcactgacg caggagggcc agggggccgg cagcagggtg	1740
cacgaattcc agacgctgtc cccggaggga tctggcaact tggcgggtat tggcggcgtg	1800
gctgtcggtg tggtcctgct tctggtgctg gcaggagttg gcttctttat ccaccgcagg	1860
aggaagaacc agcgtgcccgcag ccagtcccg gaggacgttt acttctccaa gtcagaacaa	1920
ctgaagcccc tgaagacata cgtggacccc cacacatatg aggacccaa ccaggctgtg	1980
ttgaagttca ctaccgagat ccatccatcc tggtcactc ggcagaaggt gatcggagca	2040
ggagagtttggta caagggcatg ctgaagacat cctcggggaa gaaggaggtg	2100
ccgggtggcca tcaagacgct gaaagccggc tacacagaga agcagcgagt ggacttcctc	2160
ggcgaggccg gcatcatggg ccagttcagc caccacaaca tcatccgcct agagggcgtc	2220
atctccaaat acaagcccat gatgatcatc actgagttaca tggagaatgg ggcctggac	2280
aagttccttc gggagaagga tggcgagttc agcgtgctgc agctggtgaa catgctgcgg	2340
ggcatcgcaag ctggcatgaa gtacctggcc aacatgaact atgtgcaccg tgacctggct	2400
gcccgcacaa tcctcgtaa cagcaacctg gtctgcaagg tgtctgactt tggcctgtcc	2460
cgcgtgtgg aggacgaccc cgaggccacc tacaccacca gtggcggcaa gatccccatc	2520
cgctggaccg ccccgaggcc catttcctac cggaagttca cctctgccag cgacgtgtgg	2580
agctttggca ttgtcatgtg ggaggtgatg acctatggcg agcggcccta ctgggagttg	2640
tccaaccacg aggtgatgaa agccatcaat gatggcttcc ggctccccac acccatggac	2700
tgccccctccg ccatctacca gctcatgatg cagtgcgtgc agcaggagcg tgccccccgc	2760
cccaagttcg ctgacatcgt cagcatcctg gacaagctca ttcgtcccc tgactccctc	2820
aagaccctgg ctgactttga ccccccgcgtg tctatccggc tccccagcac gagcggctcg	2880
gaggggggtgc cttccgcac ggtgtccgag tggctggagt ccatcaagat gcagcagtat	2940

acggagcact tcatggcgcc cggtacact gccatcgaga aggtggtgca gatgaccaac 3000
 gacgacatca agaggattgg ggtgcggctg cccggccacc agaagcgcat cgcctacagc 3060
 ctgctggac tcaaggacca ggtgaacact gtggggatcc ccatac 3105

<210> 20
 <211> 1035
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Predicted fusion protein
 <400> 20

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Leu Gln Ala
 50 55 60

Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala
 65 70 75 80

Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala
 85 90 95

Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp
 100 105 110

Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val
 115 120 125

Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp
 130 135 140

Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr
 145 150 155 160

Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu
 165 170 175

Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn
180 185 190

Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu
195 200 205

Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu Asn Val
210 215 220

Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala
225 230 235 240

Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr
245 250 255

Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu
260 265 270

Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr
275 280 285

Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met
290 295 300

His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu
305 310 315 320

Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser
325 330 335

Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys
340 345 350

Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys
355 360 365

Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys
370 375 380

Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly
385 390 395 400

Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg
405 410 415

Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser
 420 425 430

Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro
 435 440 445

His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His
 450 455 460

Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu
 465 470 475 480

Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr
 485 490 495

Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser
 500 505 510

Val Ser Trp Ser Ile Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr
 515 520 525

Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg
 530 535 540

Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr
 545 550 555 560

Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala
 565 570 575

Gly Ser Arg Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly
 580 585 590

Asn Leu Ala Val Ile Gly Val Ala Val Gly Val Val Leu Leu Leu
 595 600 605

Val Leu Ala Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln
 610 615 620

Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln
 625 630 635 640

Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro
 645 650 655

Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val
660 665 670

Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys
675 680 685

Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile
690 695 700

Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu
705 710 715 720

Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg
725 730 735

Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu
740 745 750

Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly
755 760 765

Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala
770 775 780

Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala
785 790 795 800

Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp
805 810 815

Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr
820 825 830

Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile
835 840 845

Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile
850 855 860

Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu
865 870 875 880

Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro
885 890 895

Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys

900

905

910

Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser
 915 920 925

Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala
 930 935 940

Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser
 945 950 955 960

Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys
 965 970 975

Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile
 980 985 990

Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val
 995 1000 1005

Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly
 1010 1015 1020

Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 1025 1030 1035

<210> 21
 <211> 1506
 <212> DNA
 <213> Homo sapiens

<400> 21	
cagggcaagg aagtggtaact gctggacttt gctgcagctg gaggggagct cggctggctc	60
acacacccgt atggcaaagg gtgggacctg atgcagaaca tcatgaatga catgccgatc	120
tacatgtact ccgtgtgcaa cgtgatgtct ggcgaccagg acaactggct cccgaccaac	180
tgggtgtacc gaggagaggc tgagcgtatc ttcattgagc tcaagttac tgtacgtgac	240
tgcaacagct tccctgggtgg cgccagctcc tgcaaggaga ctttcaacct ctactatgcc	300
gagtcggacc tggactacgg caccaacttc cagaagcgcc tggcaccaaa gattgacacc	360
attgcgcccc atgagatcac cgtcagcagc gacttcgagg cacgccacgt gaagctgaac	420
gtggaggagc gctccgtggg gccgctcacc cgcaaaggct tctacctggc cttccaggat	480
atcggtgctt gtgtggcgct gctctccgtc cgtgtctact acaagaagtg ccccgagctg	540
ctgcaggggcc tggcccactt ccctgagacc atcgccggct ctgatgcacc ttcccctggcc	600

actgtggccg gcacctgtgt ggaccatgcc gtgggccac cggggggta agagccccgt	660
atgcactgtg cagtggatgg cgagtggctg gtgccattg ggcagtgcct gtgccaggca	720
ggctacgaga aggtggagga tgcctgcag gcctgctgc ctggatttt taagtttag	780
gcatctgaga gcccctgctt ggagtgcct gagcacacgc tgccatccc tgagggtgcc	840
acctcctgcg agtgtgagga aggcttcttc cggcacccctc aggacccagc gtcgatgcct	900
tgcacacgac cccctccgc cccacactac ctcacagccg tggcatggg tgccaagggt	960
gagctgcgt ggacgcccccc tcaggacagc gggggccgcg aggacattgt ctacagcg	1020
acctgcgaac agtgtggcc cgagtctggg gaatgcggc cgtgtgaggc cagtgtgcgc	1080
tactcggagc ctcctcacgg actgaccgc accagtgtga cagtgagcga cctggagccc	1140
cacatgaact acacccac cgtggaggcc cgcaatggcg tctcaggcct ggtaaccagc	1200
cgcagcttcc gtactgccag tgtcagcatc aaccagacag agccccccaa ggtgaggctg	1260
gagggcccga gcaccaccc gcttagcg tcctggagca tccccccgc gcagcagagc	1320
cagagtgtga agtacgaggt cacttaccgc aagaagggag actccaacag ctacaatgt	1380
cgcgcaccc agggtttctc cgtgaccctg gacgacctgg ccccagacac cacctacctg	1440
gtccaggtgc aggcaactgac gcaggagggc cagggggccg gcagcagggt gcacgaattc	1500
cagacg	1506

<210> 22

<211> 1506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human sequence optimized for codon usage in Listeria

<400> 22

caaggtaaag aagttttttt attagattttt gcagcagcag gtggtaattt aggttttttta	60
acacatccat atggtaaagg ttggattta atgaaaata ttatgaatga tatgccaatt	120
tatatgtata gtgtttgtaa tgttatgagt ggtgatcaag ataattggtt acgtacaaat	180
tgggtttatc gtggtaagc agaacgtatt tttattgaat taaaatttac agttcgttat	240
tgtatagtt ttccaggtgg tgcaagttagt tgtaaagaaa catttaattt atattatgca	300
gaaagtgatt tagattatgg tacaaattttt caaaaacgtt tatattacaaa aattgataca	360
attgcaccag atgaaattac agtttagtagt gatttgaag cacgtcatgt taaattaaat	420
gttgaagaac gtgtgttgg tccattaaca cgtaaagggtt tttatattgc atttcaagat	480
attgggtcat gtgtgcatt attaagtgtt cgtgtttattt ataaaaatg tccagaattt	540

ttacaagggtt tagcacattt tccagaaaca attgcaggta gtgatgcacc aagtttagca	600
acagttgcag gtacatgtgt tgatcatgca gttgttccac caggtggtga agaaccacgt	660
atgcattgtg cagttgatgg tgaatggta gttccaattg gtcaatgttt atgtcaagca	720
ggttatgaaa aagttgaaga tgcgtcaaa gcatgttagtc caggttttt taaatttcaa	780
gcaagtgaaa gtccatgttt agaatgtcca gaacatacat taccaagtcc agaagggtgca	840
acaagttgtg aatgtgaaga aggtttttt cgtgcaccac aagatccagc aagtatgcca	900
tgtacacgtc caccaagtgc accacattat ttaacagcag ttggtatggg tgcaaaagtt	960
gaattacgtt ggacaccacc acaagatagt ggtggcgtg aagatattgt ttatagtgtt	1020
acatgtgaac aatgtggcc agaaagtggt gaatgtggtc catgtgaagc aagtgttcgt	1080
tatagtgaac caccacatgg tttaacacgt acaagtgtta cagttagtga tttagaacca	1140
catatgaatt atacatttac agttgaagca cgtaatggtg tttagtggttt agttacaagt	1200
cgtagtttc gtacagcaag tgtagtatt aatcaaacag aaccacaaa agttcggtta	1260
gaaggtcgta gtacaacaag tttaagtgtt agttggagta ttccaccacc acaacaaagt	1320
cgtgttggaaatatgaagt tacatatcgt aaaaaaggtg atagtaatag ttataatgtt	1380
cgtcgtag aaggttttag tgtagtacatta gatgatggtag caccagatac aacatattta	1440
gttcaagttc aagcattaac acaagaaggt caaggtgcag gtatcggtt tcatgaattt	1500
caaaca	1506

<210> 23
 <211> 502
 <212> PRT
 <213> Homo sapiens

<400> 23

Gln	Gly	Lys	Glu	Val	Val	Leu	Leu	Asp	Phe	Ala	Ala	Ala	Gly	Gly	Glu
1				5				10					15		

Leu	Gly	Trp	Leu	Thr	His	Pro	Tyr	Gly	Lys	Gly	Trp	Asp	Leu	Met	Gln
						20			25				30		

Asn	Ile	Met	Asn	Asp	Met	Pro	Ile	Tyr	Met	Tyr	Ser	Val	Cys	Asn	Val
							35		40			45			

Met	Ser	Gly	Asp	Gln	Asp	Asn	Trp	Leu	Arg	Thr	Asn	Trp	Val	Tyr	Arg
						50		55			60				

Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp

65

70

75

80

Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn
 85 90 95

Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys
 100 105 110

Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val
 115 120 125

Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg
 130 135 140

Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp
 145 150 155 160

Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys
 165 170 175

Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala
 180 185 190

Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp
 195 200 205

His Ala Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala
 210 215 220

Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala
 225 230 235 240

Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe
 245 250 255

Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His
 260 265 270

Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly
 275 280 285

Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro
 290 295 300

Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val
 305 310 315 320

Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile
 325 330 335

Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys
 340 345 350

Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu
 355 360 365

Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr
 370 375 380

Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser
 385 390 395 400

Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro
 405 410 415

Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp
 420 425 430

Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr
 435 440 445

Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu
 450 455 460

Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu
 465 470 475 480

Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg
 485 490 495

Val His Glu Phe Gln Thr
 500

<210> 24

<211> 1689

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein construct

<400> 24

atgaaaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60

caaactgaag	caaaggatgc	atctgcattc	aataaagaaa	attcaatttc	atccatggca	120
ccaccagcat	ctccgcctgc	aagtccctaag	acgccaatcg	aaaagaaaaca	cgcggatctc	180
gagcagggca	aggaagtgg	actgctggac	tttgctgcag	ctggagggga	gctcggtcg	240
ctcacacacc	cgtatggcaa	agggtggac	ctgatgcaga	acatcatgaa	tgacatgcg	300
atctacatgt	actccgtgt	caacgtgatg	tctggcgacc	aggacaactg	gctccgcacc	360
aactgggtgt	accgaggaga	ggctgagcgt	atcttcattg	agctcaagtt	tactgtacgt	420
gactgcaaca	gcttccctgg	tggcgccagc	tcctgcaagg	agactttcaa	cctctactat	480
gccgagtcgg	acctggacta	cggcaccaac	ttccagaagc	gcctgttac	caagattgac	540
accattgcgc	ccgatgagat	caccgtcagc	agcgacttcg	aggcacgcca	cgtgaagctg	600
aacgtggagg	agcgctccgt	ggggccgctc	acccgcaaag	gcttctacct	ggccttccag	660
gatatcggtg	cctgtgtggc	gctgctctcc	gtccgtgtct	actacaagaa	gtgccccgag	720
ctgctgcagg	gcctggccca	cttccctgag	accatcgccg	gctctgatgc	accttccctg	780
gccactgtgg	ccggcacctg	tgtggaccat	gccgtggtgc	caccgggggg	tgaagagccc	840
cgtatgcact	gtgcagtgga	tggcgagtgg	ctggtgccca	ttggcagtg	cctgtgccag	900
gcaggctacg	agaaggtgga	ggatgcctgc	caggcctgct	cgcctggatt	tttaagtt	960
gaggcatctg	agagccccctg	cttggagtgc	cctgagcaca	cgctgccatc	ccctgagggt	1020
gccacctcct	gcgagtgtga	ggaaggcttc	ttccgggcac	ctcaggaccc	agcgtcgatg	1080
ccttgcacac	gaccggccctc	cgccccacac	tacctcacag	ccgtggcat	gggtgccaag	1140
gtggagctgc	gctggacgccc	ccctcaggac	agcgggggccc	gcgaggacat	tgtctacagc	1200
gtcacctgcg	aacagtgtgc	gccccgatct	gggaaatgcg	ggccgtgtga	ggccagtg	1260
cgctactcgg	agcctcctca	cggactgacc	cgcaccagt	tgacagtgag	cgacctggag	1320
ccccacatga	actacacatt	caccgtggag	gcccgaatg	gcgtctcagg	cctggtaacc	1380
agccgcagct	tccgtactgc	cagtgtcagc	atcaaccaga	cagagcccc	caaggtgagg	1440
ctggagggcc	gcagcaccac	ctcgcttagc	gtctcctgg	gcatcccc	gccgcagcag	1500
agccgagtgt	ggaagtacga	ggtcacttac	cgcaagaagg	gagactccaa	cagctacaat	1560
gtgcgcgcga	ccgagggttt	ctccgtgacc	ctggacgacc	tggccccaga	caccacctac	1620
ctggtccagg	tgcaggcact	gacgcaggag	ggccaggggg	ccggcagcag	ggtgcacgaa	1680
ttccagacg						1689

<210> 25

<211> 563

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 25

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Gln Gly Lys
50 55 60

Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp
65 70 75 80

Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met
85 90 95

Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly
100 105 110

Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala
115 120 125

Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser
130 135 140

Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr
145 150 155 160

Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe
165 170 175

Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp
180 185 190

Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly
195 200 205

Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala
210 215 220

Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu
225 230 235 240

Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp
245 250 255

Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala Val
260 265 270

Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp Gly
275 280 285

Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu
290 295 300

Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe
305 310 315 320

Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro
325 330 335

Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg
340 345 350

Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala
355 360 365

Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg
370 375 380

Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser
385 390 395 400

Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys
405 410 415

Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr
420 425 430

Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr
435 440 445

Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe
450 455 460

Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg
 465 470 475 480

Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro
 485 490 495

Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys
 500 505 510

Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser
 515 520 525

Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val
 530 535 540

Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His Glu
 545 550 555 560

Phe Gln Thr

<210> 26
 <211> 1989
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 26	60
ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaa	60
atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcgtt tcatcttag aagcgaattt cgccaatatt ataattatca aaagagaggg	180
gtggcaaacg gtatggca ttattagtt aaaaaatgta gaaggagagt gaaacccatg	240
aaaaaaataa tgctagttt tattacactt atattagtta gtctaccaat tgcgcaacaa	300
actgaagcaa aggatgcattc tgcattcaat aaagaaaatt caatttcattc catggcacca	360
ccagcatctc cgcctgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc	420
gattataaaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttgcagca	480
gcaggtggtg aattaggttg gttaacacat ccatatggta aagggtggaa ttatgcaa	540
aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtggat	600
caagataatt gttacgtac aaattgggtt tattcgtggtg aagcagaacg tattttatt	660

gaattaaaaat ttacagttcg tgattgtaat agtttccag gtggtgcaag tagttgtaaa 720
gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa tttcaaaaa 780
cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840
gaagcacgtc atgttaaatt aaatgtgaa gaacgttagtgc ttggccatt aacacgtaaa 900
ggttttatt tagcatttca agatattggc gcatgtgttgc cattattaag tggtcggtt 960
tattataaaa aatgtccaga attattacaa ggtttagcac attttccaga aacaattgca 1020
ggtagtgatg caccaagttt agcaacagtt gcaggtacat gtgttgcata tgcaagttgtt 1080
ccaccagggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gtttagttcca 1140
attggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcattg tcaagcatgt 1200
agtccaggtt ttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat 1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt tttcggtca 1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca 1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtggtggt 1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggcagaaag tggtgaatgt 1500
ggtccatgtg aagcaagtgt tcgttatagt gaaccaccac atggtttaac acgtacaagt 1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat 1620
ggtgttagtg gtttagttac aagtcgttagt ttgcgtacag caagtgttag tattaatcaa 1680
acagaaccac caaaaagttcg tttagaaggt cgtagtacaa caagtttaag tgtagttgg 1740
agtattccac caccacaaca aagtcgtgtt tggaaatatg aagttacata tcgtaaaaaaa 1800
ggtgatagta atagttataa tggtcggtcgt acagaaggttt tagtgttac attagatgt 1860
tttagcaccag atacaacata ttttagttcaa gttcaaggcat taacacaaga aggtcaaggt 1920
gcaggttagtc gtgttcatgaa atttcaaaca gaacaaaaat taatttagtga agaagattta 1980
tgagagctc 1989

<210> 27
<211> 581
<212> PRT
<213> Artificial Sequence

<220>

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala
65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly
85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr
100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr
115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys
130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys
145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly
165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro
180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu
195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr
210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg
225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe
245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala
260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro
275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln
290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala
305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu
325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys
340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met
355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly
370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly
385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro
405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu
420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu
435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser
450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn
465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser
485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Gln Gln Ser Arg Val Trp

500

505

510

Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn
 515 520 525

Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro
530 535 540

Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln
545 550 555 560

Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile
 565 570 575

Ser Glu Glu Asp Leu
580

<210> 28
<211> 1989
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Construct for fusion protein

<400> 28
ggtacccctt tgatttagta tattcctatc ttaaaagttac ttttatgtgg aggcattaaac 60
atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaaag caagcatata 120
atattgcgtt tcatctttag aagcgaattt cgccaatatt ataatttatca aaagagaggg 180
gtggcaaaccg gtatttggca ttatttagtt aaaaaatgtt gaaggagagt gaaacccatg 240
aaaaaaaaatta tgtagtttt tattacatta attttagtta gtttaccaat tgcacaacaa 300
acagaagcaa aagatgcaag tgcatttaat aaagaaaata gtatttagttag tatggcacca 360
ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc 420
gattataaag atgatgatga taaacaaggt aaagaagttg ttttattttaga ttttgcagca 480
gcaggtggtg aatttaggtt gtttacacat ccatatggta aaggtggga ttttgcacaa 540
aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtgggtat 600
caagataatt gtttacgtac aaattgggtt ttttgcacaa aagcagaacg tattttattt 660
gaattttttttt ttttgcacaa aatgtttttt ttttgcacaa aatgtttttt ttttgcacaa 720
gaaacattta atttatatta ttttgcacaa aatgtttttt ttttgcacaa aatgtttttt 780
cgtttattta caaaaattttt ttttgcacaa aatgtttttt ttttgcacaa aatgtttttt 840
gaagcacgtc atgtttttttt aatgtttttt ttttgcacaa aatgtttttt ttttgcacaa 900

ggtttttatt tagcatttca agatatttgt gcatgtgttgcattattaag tgttcggtt	960
tattataaaa aatgtccaga attattacaa gtttagcac atttccaga aacaattgca	1020
ggtagtgatg caccaagttt agcaacagtt gcaggtacat gtgttgcata tgcagtttt	1080
ccaccagggtg gtgaagaacc acgtatgcat tgtgcagttg atggtaatg gttagttcca	1140
attggtaat gtttatgtca agcaggttat gaaaaagttt aagatgcata tcaagcatgt	1200
agtccaggtt ttttaaatt tgaagcaagt gaaagtccat gttagaatg tccagaacat	1260
acattacaa gtccagaagg tgcaacaagt tgtgaatgtt aagaaggttt tttcgtgca	1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaaa gtgcaccaca ttatttaaca	1380
gcagttggta tgggtgcaaa agttgaatata cgttggacac caccacaaga tagtgggtgt	1440
cgtgaagata ttgttatag ttttacatgtt gaacaatgtt ggccagaaag tggtaatgt	1500
ggtccatgtt aagcaagtgt tcgttatagt gaaccaccac atggtttac acgtacaagt	1560
tttacagtta gtgatttata accacatatg aattatacat ttacagttga agcagtaat	1620
ggtgttagtgcgtttagttac aagtcgttgtt ttccgtacag caagtgttag tattatcaa	1680
acagaaccac caaaagttcg ttttagaaggt cgtgtacaa caagttaag ttttagttgg	1740
agtattccac caccacaaca aagtcgtgtt tggaaatatg aagttacata tcgtaaaaaaaa	1800
ggtgatagta atagttataa ttttcgtcgtt acagaaggtt ttagtgttac attagatgt	1860
tttagcaccat atacaacata ttttagttcaaa gttcaagcat taacacaaga aggtcaaggt	1920
gcaggttagtc gtgttcatgttcaaaaca gaacaaaaat taatttagtga agaagattta	1980
tgagagctc	1989

<210> 29
 <211> 581
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Predicted Fusion protein
 <400> 29

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala
65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly
85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr
100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr
115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys
130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys
145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly
165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro
180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu
195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr
210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg
225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe
245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala
260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro
275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln
 290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala
 305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu
 325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys
 340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met
 355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly
 370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly
 385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro
 405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu
 420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu
 435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser
 450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn
 465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser
 485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp
 500 505 510

Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn
 515 520 525

Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro
 530 535 540

Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln
 545 550 555 560

Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile
 565 570 575

Ser Glu Glu Asp Leu
 580

<210> 30
 <211> 1968
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 30	60
ggtacccctt tgattagta tattcctatc taaaagttac ttttatgtgg aggcattaaac	
atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcgtt tcatttttag aagcgaattt cgccaatatt ataattatca aaagagaggg	180
gtggcaaacg gtatttggca ttattagtt aaaaaatgta gaaggagagt gaaacccatg	240
gcatacgcaca gtcgtttga tgaatggta cagaaactga aagaggaaag ctttcaaaac	300
aatacgtttg accggcgcaa atttattcaa ggagcgggaa agattgcagg actttcttt	360
ggattaaacg ttgtccagtc ggttggggcc tttggatccg attataaaga tgatgtat	420
aaacaaggta aagaagttgt tttattagat tttgcagcag caggtggta attaggttg	480
ttaacacatc catatggtaa aggtggat ttaatgcaaa atattatgaa tgatatgcca	540
atttatatgt atagtgtttg taatgttatg agtggtgatc aagataattt gttacgtaca	600
aattgggttt atcgtggta agcagaacgt atttttattt aattttttt tacagttcg	660
gattgtataa gtttccagg tggtgcaagt agttgtaaag aaacattaa tttatattt	720
gcagaaaatg atttagatta tggtacaaat tttcaaaaac gtttatttac aaaaattgt	780
acaattgcac cagatgaaat tacagttgt agtgattttg aagcacgtca tggtaattt	840
aatgttgaag aacgtgtgt tggtccatta acacgtaaag gttttttttt agcatttcaa	900
gatattggtg catgtgtgc attattaagt gttcgtgtt attataaaaa atgtccagaa	960
ttattacaag gtttagcaca tttccagaa acaattgcag gtgtgtgc accaagttt	1020
gcaacagttg caggtacatg tggatcat gcaagggttc caccaggtgg tgaagaacca	1080

cgtatgcatt	gtgcagttga	tggtaatgg	ttagttccaa	ttggtaatg	tttatgtcaa	1140
gcaggttatg	aaaaagttga	agatgcattgt	caagcatgt	gtccagggtt	ttttaaattt	1200
gaagcaagt	aaagtccatg	tttagaatgt	ccagaacata	cattaccaag	tccagaaggt	1260
gcaacaagtt	gtgaatgtga	agaaggttt	tttcgtgcac	cacaagatcc	agcaagtatg	1320
ccatgtacac	gtccaccaag	tgcaccacat	tatttaacag	cagttggat	gggtgcaaaa	1380
gttgaattac	gttggacacc	accacaagat	agtggggc	gtgaagat	tgttatagt	1440
gttacatgt	aacaatgtt	gccagaaagt	ggtgaatgt	gtccatgt	agcaagtgtt	1500
cgttatag	aaccaccaca	tggtttaca	cgtacaagt	ttacagtt	tgatttagaa	1560
ccacatatga	attatacatt	tacagttgaa	gcacgtaatg	gtgttagtgg	tttagttaca	1620
agtcgttagt	ttcgtacagc	aagtgttagt	attaatcaa	cagaaccacc	aaaagttcg	1680
ttagaagg	tcgtacaac	aagttaagt	gttagttgga	gtattccacc	accacaacaa	1740
agtcgtgtt	gaaaatatga	agttacat	cgtaaaaaag	gtgatagtaa	tagttataat	1800
ttcgtcgta	cagaagg	ttttagttaca	ttagatgatt	tagcaccaga	tacaacat	1860
ttagttcaag	ttcaagcatt	aacacaagaa	ggtcaaggt	caggtagtc	tgttcatgaa	1920
tttcaaacag	aacaaaaatt	aattagt	gaa	gaagattt	gagagctc	1968

<210> 31
 <211> 574
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion Protein

<400> 31

Met	Ala	Tyr	Asp	Ser	Arg	Phe	Asp	Glu	Trp	Val	Gln	Lys	Leu	Lys	Glu
1									10					15	

Glu	Ser	Phe	Gln	Asn	Asn	Thr	Phe	Asp	Arg	Arg	Lys	Phe	Ile	Gln	Gly
													20	25	30

Ala	Gly	Lys	Ile	Ala	Gly	Leu	Ser	Leu	Gly	Leu	Thr	Ile	Ala	Gln	Ser
												35	40	45	

Val	Gly	Ala	Phe	Gly	Ser	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Gln	Gly
												50	55	60	

Lys	Glu	Val	Val	Leu	Leu	Asp	Phe	Ala	Ala	Gly	Gly	Glu	Leu	Gly	
												65	70	75	80

Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile
85 90 95

Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser
100 105 110

Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu
115 120 125

Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn
130 135 140

Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr
145 150 155 160

Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu
165 170 175

Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser
180 185 190

Asp Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val
195 200 205

Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly
210 215 220

Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro
225 230 235 240

Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser
245 250 255

Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala
260 265 270

Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp
275 280 285

Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr
290 295 300

Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys
305 310 315 320

Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu
 325 330 335

Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Gly Phe Phe
 340 345 350

Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser
 355 360 365

Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu
 370 375 380 385

Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr
 385 390 395 400

Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro
 405 410 415

Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg
 420 425 430

Thr Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe
 435 440 445

Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser
 450 455 460 480

Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val
 465 470 475 480

Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile
 485 490 495

Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg
 500 505 510

Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe
 515 520 525

Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln
 530 535 540

Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His
 545 550 555 560

Glu Phe Gln Thr Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

565

570

<210> 32
 <211> 1254
 <212> DNA
 <213> Homo sapiens

<400> 32

caccgcagga ggaagaacca gcgtccccgc cagtccccgg aggacgttta cttctccaag	60
tcagaacaac tgaagccctt gaagacatac gtggacccccc acacatatga ggaccccaac	120
caggctgtgt tgaagttcac taccgagatc catccatcct gtgtcactcg gcagaaggtg	180
atcggagcag gagagtttg ggaggtgtac aagggcatgc tgaagacatc ctcgggaaag	240
aaggaggtgc cggtgccat caagacgctg aaagccggct acacagagaa gcagcgagt	300
gacttcctcg gcgaggccgg catcatgggc cagttcagcc accacaacat catccgccta	360
gagggcgtca tctccaaata caagccatg atgatcatca ctgagttacat ggagaatgg	420
gccctggaca agttcctcg ggagaaggat ggcgagttca gcgtgctgca gctgggtggc	480
atgctgcggg gcatcgac tggcatgaag tacctggcca acatgaacta tgtgcaccgt	540
gacctggctg cccgcaacat cctcgtcaac agcaacctgg tctgcaaggt gtctgacttt	600
ggcctgtccc gcgtgctgga ggacgacccc gaggccacct acaccaccag tggcggcaag	660
atccccatcc gctggaccgc cccggaggcc atttcctacc ggaagttcac ctctgcccagc	720
gacgtgtgga gcttggcat tgtcatgtgg gaggtgatga cctatggcga gcggccctac	780
tgggagttgt ccaaccacga ggtgatgaaa gccatcaatg atggcttccg gctccccaca	840
cccatggact gcccctccgc catctaccag ctcatgatgc agtgcgtggca gcaggagcgt	900
gcccggccccc ccaagttcgc tgacatcgac agcatcctgg acaagctcat tcgtgcccct	960
gactccctca agaccctggc tgactttgac ccccgctgt ctatccggct ccccagcactg	1020
agcggctcgg agggggtgcc cttccgcacg gtgtccgagt ggctggagtc catcaagatg	1080
cagcagtata cggagcactt catggcggcc ggctacactg ccacgagaa ggtggcgtcag	1140
atgaccaacg acgacatcaa gaggattggg gtgcggctgc cggccacca gaagcgcac	1200
gcctacagcc tgctggact caaggaccag gtgaacactg tggggatccc catc	1254

<210> 33
 <211> 1254
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sequence Optimized for codon usage in Listeria

<400> 33
 cacagacgta gaaaaaatca acgtgctcga caatccccag aagatgtgta ttttcgaaa 60
 agtgaacaat taaaaccatt aaaaacttat gttgatccgc atacgtacga agacccaaat 120
 caagcagtat taaaattac aacagaaata caccaagtt gtgttacaag acaaaaagtt 180
 attggagcag gtgaattcgg agaggtatat aaaggtatgt taaaaacatc atcaggtaaa 240
 aaagaagttc cggttgcaat taaaacctta aaggcaggat atacagaaaa acagcgagtt 300
 gatttttag gtgaagcagg aattatgggt caatttagcc atcataatat tattcgtttg 360
 gaaggagtaa taagtaaata taaaccaatg atgattatta cagaatacat gaaaaacggt 420
 gcttagata aattttacg tgaaaaggat ggtgaattta gtgtttaca attgggttgt 480
 atgttaagag gaattgctgc aggtatgaaa tatttagcta atatgaatta tgttcaccgt 540
 gatttggcag caagaaatat cctagtcaat tccaaatttag tatgtaaagt tagtgattt 600
 ggtttaagca gagtattaga agacgatcca gaggcaacct atacaacatc gggaggtaaa 660
 attcctattc gttggacagc accagaagct atcagttacc gtaaatttac aagtgcacca 720
 gacgtgtgga gtttggat tgtaatgtgg gaagttatga catatggaga aagaccatata 780
 tgggaattaa gtaatcatga agttatgaaa gcaattaacg atggatttag attaccaact 840
 ccgatggatt gtccatctgc catttatcaa ctaatgatgc aatgttggca acaagaaaaga 900
 gcacgacgtc caaaatttgc agatattgtt agtatttag acaaattaat tcgtgcacca 960
 gatagtttaa aaactttgc agactttgat cctcgtgtta gtattcgatt accaagtacg 1020
 tcaggttccg aaggagttcc atttcgcaca gtctccgaat ggttggaaatc aattaaaatg 1080
 caacaataca cgcacactt tatggcagca gtttacacag caatcgaaaa agttgttcaa 1140
 atgacaaatg atgatattaa acgtattgga gtttagattac caggccacca gaaacgtatt 1200
 gcatattctt tattaggttt aaaagatcaa gttaataccg tggaaattcc aatt 1254

<210> 34
 <211> 456
 <212> PRT
 <213> Homo sapiens

<400> 34

Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala
 1 5 10 15

Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu Ala
 20 25 30

Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln Arg Ala Arg
 35 40 45

Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro
50 55 60

Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala
65 70 75 80

Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln
85 90 95

Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu
100 105 110

Lys Thr Ser Ser Gly Lys Glu Val Pro Val Ala Ile Lys Thr Leu
115 120 125

Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala
130 135 140

Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly
145 150 155 160

Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu
165 170 175

Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser
180 185 190

Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys
195 200 205

Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn
210 215 220

Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu
225 230 235 240

Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly
245 250 255

Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg
260 265 270

Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp
275 280 285

Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His
 290 295 300

Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met
 305 310 315 320

Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln
 325 330 335

Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp
 340 345 350

Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp
 355 360 365

Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val
 370 375 380

Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln
 385 390 395 400

Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val
 405 410 415

Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro
 420 425 430

Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln
 435 440 445

Val Asn Thr Val Gly Ile Pro Ile
 450 455

<210> 35

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein

<400> 35
 atgaaaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60
 caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
 ccaccagcat ctccgcctgc aagtccctaag acgccaatcg aaaagaaaaca cgcgatctc 180

gagcaccgca	ggaggaagaa	ccagcgtgcc	cgcgcgtccc	cgaggacgt	ttacttctcc	240
aagtcaaac	aactgaagcc	cctgaagaca	tacgtggacc	cccacacata	tgaggacccc	300
aaccaggctg	tgttgaagtt	cactaccgag	atccatccat	cctgtgtcac	tcggcagaag	360
gtgatcggag	caggagagtt	tggggaggtg	tacaaggca	tgctgaagac	atcctcgggg	420
aagaaggagg	tgccgggtggc	catcaagacg	ctgaaagccg	gctacacaga	gaagcagcga	480
gtggacttcc	tcggcgaggc	cggcatcatg	ggccagttca	gccaccacaa	catcatccgc	540
ctagagggcg	tcatctccaa	atacaaggcc	atgatgatca	tcactgagta	catggagaat	600
ggggccctgg	acaagttcct	tcgggagaag	gatggcgagt	tcagcgtgct	gcagctggtg	660
ggcatgctgc	ggggcatcgc	agctggcatg	aagtacctgg	ccaacatgaa	ctatgtgcac	720
cgtgacctgg	ctgcccgc当地	catcctcgctc	aacagcaacc	tggtctgcaa	ggtgtctgac	780
tttggcctgt	cccgcggtgct	ggaggacgac	cccggaggcca	cctacaccac	cagtggcggc	840
aagatccccca	tccgctggac	cgccccggag	gccatttcct	accggaagtt	cacctctgcc	900
agcgacgtgt	ggagctttgg	cattgtcatg	tggaggtga	tgacctatgg	cgagcggccc	960
tactggaggt	tgtccaaacca	cgaggtgatg	aaagccatca	atgatggctt	ccggctcccc	1020
acacccatgg	actgcccctc	cgccatctac	cagctcatga	tgcagtgctg	gcagcaggag	1080
cgtccccgcc	gcccccaagtt	cgctgacatc	gtcagcatcc	tggacaagct	cattcgtgcc	1140
cctgactccc	tcaagaccct	ggctgacttt	gaccccccgc当地	tgtctatccg	gctccccagc	1200
acgagcggct	cggaggggggt	gcccttccgc	acggtgtccg	agtggctgga	gtccatcaag	1260
atgcagcagt	atacggagca	cttcatggcg	gccggctaca	ctgccatcga	gaaggtggtg	1320
cagatgacca	acgacgacat	caagaggatt	ggggtgcggc	tgccccc当地	ccagaagcgc	1380
atcgctaca	gcctgctggg	actcaaggac	caggtgaaca	ctgtgggat	ccccatc	1437

<210> 36
 <211> 479
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Predicted Protein Sequence
 <400> 36

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu His Arg Arg
50 55 60

Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser
65 70 75 80

Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr
85 90 95

Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His
100 105 110

Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly
115 120 125

Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val
130 135 140

Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg
145 150 155 160

Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His
165 170 175

Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met
180 185 190

Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg
195 200 205

Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg
210 215 220

Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His
225 230 235 240

Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys
245 250 255

Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu
260 265 270

Ala Thr Tyr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala
275 280 285

Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp
290 295 300

Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro
305 310 315 320

Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly
325 330 335

Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu
340 345 350

Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala
355 360 365

Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu
370 375 380

Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser
385 390 395 400

Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu
405 410 415

Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly
420 425 430

Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys
435 440 445

Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser
450 455 460

Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
465 470 475

<210> 37
<211> 1737
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein sequence

<400> 37

ggcacccct ttgatttagta tattcctatc taaaagttac ttttatgtgg aggcattaac 60
atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
atattgcgtt tcatctttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180

gtggcaaacg gtatttgca ttatttagtt aaaaaatgta gaaggagagt gaaaccatg 240
aaaaaaataa tgctagttt tattacactt atattagtt gtctaccaat tgcgcaacaa 300
actgaagcaa aggatgcac tgcattcaat aaagaaaatt caatttcacat gatggcacca 360
ccagcatctc cgccctgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc 420
gattataaag atgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc 480
ccagaagatg tgtattttc gaaaagtgaa caattaaaac cattaaaaac ttatgttgat 540
ccgcatacgt acgaagaccc aaatcaagca gtattaaaat ttacaacaga aatacaccca 600
agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaaggt 660
atgttaaaaa catcatcagg taaaaaagaa gttccgggtt caattaaaac cttaaaggca 720
ggatatacag aaaaacagcg agttgatttt ttaggtgaag caggaattat gggtcaattt 780
agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt 840
attacagaat acatggaaaa cggtgctta gataaatttt tacgtaaaaa ggatggtaa 900
tttagtgttt tacaatttgtt tggtatgtta agaggaattt ctgcaggtat gaaatattt 960
gctaataatga attatgttca ccgtgatttgc gcagcaagaa atatcctagt caattccat 1020
ttagtagtga aagtttagtga ttttggtta agcagagtat tagaagacga tccagaggca 1080
acctatacaa catcgggagg taaaattcct attcgttggc cagcaccaga agctatcagt 1140
taccgtaaat ttacaagtgc atcagacgtg tggagtttgc ggattgttaat gtgggaagtt 1200
atgacatatg gagaaagacc atattggaa ttaagtaatc atgaagttat gaaagcaatt 1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccatttcaactaatg 1320
atgcaatgtt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagttt 1380
tttagacaaat taattcgtgc accagatagt taaaaaactt tagcagactt tgatcctcgt 1440
gttagtatttgc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc 1500
gaatgggttgg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac 1560
acagcaatcg aaaaagttgt tcaaattgaca aatgatgata taaaacgtat tggagttaga 1620
ttaccaggcc accagaaacg tattgcataat tctttatttag gttaaaaaga tcaagttat 1680
accgtgggaa ttccaatttgc acaaaaaatta atttccgaag aagacttata agagctc 1737

<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Predicted fusion protein
<400> 38

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
50 55 60

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln
65 70 75 80

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu
85 90 95

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val
100 105 110

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys
115 120 125

Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys
130 135 140

Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys
145 150 155 160

Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly
165 170 175

Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val
180 185 190

Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn
195 200 205

Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val
210 215 220

Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr
225 230 235 240

Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
245 250 255

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser
260 265 270

Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Ser Gly Gly
275 280 285

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys
290 295 300

Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu
305 310 315 320

Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu
325 330 335

Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp
340 345 350

Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu
355 360 365

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys
370 375 380 385

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro
385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro
405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr
420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val
435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly

450

455

460

His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val
 465 470 475 480

Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp
 485 490 495

Leu

<210> 39
 <211> 1737
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 39	60
ggtacccctt tgatttagta tattcctatc tttaagttac ttttatgtgg aggcattaaac	120
atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaaag caagcatata	180
atattgcgtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg	240
gtggcaaacg gtatttggca ttatttagtt aaaaaatgtt gaaggagagt gaaacccatg	300
aaaaaaaaatta tgtagttt tattacatta atttttagttt gtttaccaat tgcacaacaa	360
acagaagcaa aagatgcaag tgcatttaat aaagaaaata gtatttagtag tatggcacca	420
ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc	480
gattataaag acgatgatga taaacacaga cgtaaaaaa atcaacgtgc tcgacaatcc	540
ccagaagatg tgtattttc gaaaagtgtt caattaaaac cattaaaaac ttatgttgat	600
ccgcatacgt acgaagaccc aaatcaagca gtattaaaat ttacaacaga aatacaccca	660
agttgttta caagacaaaa agttatttgc gcaggtaat tcggagaggt atataaaggt	720
atgttaaaaaa catcatcagg taaaaaagaa gttccggttt caattaaaac cttaaaggca	780
ggatatacag aaaaacagcg agttgatttt ttaggtgtt caggaattat gggtaattt	840
agccatcata atattattcg tttggaaagga gtaataagta aatataaacc aatgtatgatt	900
attacagaat acatggaaaaa cggtgcttta gataaatttt tacgtaaaaa ggatgggtt	960
tttagtgttt tacaatttggt tggtatgttta agaggaattt ctgcaggtat gaaatattt	1020
gctaataatga attatgttca ccgtgatttgc agcaagaa atatcctagt caattccat	1080
tttagtatgttta aagtttagtga ttttggttta agcagagtat tagaagacga tccagaggca	1140
acctatacaa catcgggagg taaaattccctt attcggttgc cagcaccaga agctatcgt	

taccgtaaat ttacaagtgc atcagacgtg tggagtttg ggattgtaat gtgggaagtt	1200
atgacatatg gagaaaagacc atattggaa ttaagtaatc atgaagttat gaaagcaatt	1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg	1320
atgcaatgtt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagtatt	1380
ttagacaaat taattcgtgc accagatagt taaaaaactt tagcagactt tgatcctcg	1440
gttagtattc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc	1500
gaatggttgg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac	1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaacgtat tggagttaga	1620
ttaccaggcc accagaaacg tattgcatat tctttattag gttaaaaga tcaagttaat	1680
accgtggaa ttccaattga acaaaaatta attccgaag aagacttata agagctc	1737

<210> 40

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion Protein

<400> 40

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu	
1	5
	10
	15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys	
20	25
	30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser	
35	40
	45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys	
50	55
	60

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln	
65	70
	75
	80

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu	
85	90
	95

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val	
100	105
	110

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys	
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115

120

125

Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys
 130 135 140

Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys
 145 150 155 160

Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly
 165 170 175

Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val
 180 185 190

Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn
 195 200 205

Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val
 210 215 220

Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr
 225 230 235 240

Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 245 250 255

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser
 260 265 270

Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Ser Gly Gly
 275 280 285

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys
 290 295 300

Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu
 305 310 315 320

Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu
 325 330 335

Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp
 340 345 350

Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu
 355 360 365

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys
370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro
385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro
405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr
 420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val
435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly
 450 455 460

His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val
465 470 475 480

Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp
485 490 495

Leu

aaacacagac	gtagaaaaaa	tcaacgtgct	cgacaatccc	cagaagatgt	gtatTTTCG	480
aaaagtgaac	aattaaaacc	attaaaaact	tatgttgatc	cgcatacgta	cgaagaccca	540
aatcaagcag	tattaaaatt	tacaacagaa	atacacccaa	gttgtttac	aagacaaaaaa	600
gttattggag	caggtgaatt	cgagaggtta	tataaaggta	tgtaaaaac	atcatcaggt	660
aaaaaagaag	ttccgggtgc	aattaaaacc	ttaaaggcag	gatatacaga	aaaacagcga	720
gttggatTTT	taggtgaagc	aggaattatg	ggtcaattta	gccatcataa	tattattcgt	780
tttggaggag	taataagttaa	atataaacc	atgatgatta	ttacagaata	catggaaaac	840
ggtgctttag	ataaaatttt	acgtaaaaag	gatggtaat	ttagtgttt	acaattgggt	900
ggtatgttaa	gaggaattgc	tgcaggtatg	aaatatttag	ctaataatgaa	ttatgttcac	960
cgtgatttgg	cagcaagaaa	tatcctagtc	aattccaatt	tagtatgtaa	agtttagtgt	1020
tttggtttaa	gcagagtatt	agaagacgat	ccagaggcaa	cctatacaac	atcggggaggt	1080
aaaattccta	ttcggtggac	agcaccagaa	gctatcagtt	accgtaaatt	tacaagtgc	1140
tcagacgtgt	ggagtttgg	gattgtaatg	tggaaagtta	tgacatatgg	agaaagacca	1200
tattgggaat	taagtaatca	tgaagttatg	aaagcaatta	acgatggatt	tagattacca	1260
actccgatgg	attgtccatc	tgccatttat	caactaatga	tgcaatgtt	gcaacaagaa	1320
agagcacgac	gtccaaaatt	tgcagatatt	gttagtattt	tagacaaatt	aattcgtgc	1380
ccagatagtt	taaaaacttt	agcagacttt	gatcctcgt	ttagtattcg	attaccaagt	1440
acgtcaggtt	ccgaaggagt	tccatttcgc	acagtctccg	aatggggaa	atcaattaaa	1500
atgcaacaat	acaccgaaca	ctttatggca	gcaggttaca	cagcaatcga	aaaagttgt	1560
caaatgacaa	atgatgat	taaacgtatt	ggagtttagat	taccaggcca	ccagaaacgt	1620
attgcattt	ctttatttagg	tttaaaagat	caagttataa	ccgtggaaat	tccaattgaa	1680
caaaaattaa	tttccgaaga	agacttataa	gagctc			1716

<210> 42
 <211> 490
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Predicted fusion protein
 <400> 42

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
 1 5 10 15

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly

20

25

30

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser
35 40 45

Val Gly Ala Phe Gly Ser Asp Tyr Lys Asp Asp Asp Asp Lys His Arg
50 55 60

Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe
65 70 75 80

Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His
85 90 95

Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
100 105 110

His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
115 120 125

Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
130 135 140

Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln
145 150 155 160

Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His
165 170 175

His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
180 185 190

Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu
195 200 205

Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu
210 215 220

Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
225 230 235 240

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
245 250 255

Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
260 265 270

Glu Ala Thr Tyr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
275 280 285

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
290 295 300

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
305 310 315 320

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
325 330 335

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
340 345 350

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
355 360 365

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
370 375 380

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
385 390 395 400

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
405 410 415

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
420 425 430

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
435 440 445

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
450 455 460

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
465 470 475 480

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
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<210> 43
<211> 9808
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein Construct

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<211> 26

<212> PRT

<213> Listeria monocytogenes

<400> 44

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20	25

<210> 45

<211> 59

<212> PRT

<213> Listeria monocytogenes

<400> 45

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20	25		30
	30		

Ala Gly Thr Gly Ile Ala Val Gly Ala Thr Gly Leu Gly Thr Ile Leu	
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35

40

45

Asn Val Val Asp Gln Val Asp Lys Ala Leu Thr
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<210> 46
<211> 53
<212> PRT
<213> **Bacillus subtillus**

<400> 46

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
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35 40 45

Val Gly Ala Phe Gly
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<210> 47
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
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<210> 48
<211> 24
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 48
acataatcag tccaaagtag atgc 24

<210> 49
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
ctctggtacc tcctttgatt agtatattc

29

<210> 50
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
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29

<210> 51
<211> 24
<212> DNA
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<220>
<223> Description of Artificial Sequence: Epitope insert

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gattataaaag atgatgatga taaa

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<210> 52
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epitope

<400> 52

Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epitope insert

<400> 53
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<210> 54
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<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epitope

<400> 54

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
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<210> 55

<211> 9

<212> PRT

<213> Mus sp.

<400> 55

Ser Pro Ser Tyr Val Tyr His Gln Phe
1 5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epitope

<400> 56

Ser Pro Ser Tyr Ala Tyr His Gln Phe
1 5

<210> 57

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 57

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<210> 58

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 59

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 59

atttctcgag tccatgggg gttctcatca tc

32

<210> 60

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 60

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25

<210> 61

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 61

cgattccct agttatgttt accaccaatt tgctgca

37

<210> 62

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 62

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31

<210> 63

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epitope insert

<400> 63

agtccaagtt atgcatatca tcaattt

27

<210> 64

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 64

cgatagtcga agttatgcattatcaatt tgc

33

<210> 65

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 65

gtcgcaaattt gatgatatgcataaacttgaa ctat

34

<210> 66

<211> 8

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus Sequence

<220>

<221> misc_feature

<222> (1)..(1)

<223> n is a, c, g, or u

<400> 66

naggaggu

8

<210> 67

<211> 19

<212> DNA

<213> Listeria monocytogenes

<400> 67

aaggagagtg aaacccatg

19

<210> 68

<211> 240

<212> DNA

<213> Listeria monocytogenes

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60

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120

atattgcgtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg

180

gtggcaaacg gtatttggca ttatttagtt aaaaaatgtaa gaaggagagt gaaacccatg

240

<210> 69
<211> 240
<212> DNA
<213> Listeria monocytogenes

<400> 69
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atattgcgtt tcatcttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
gtggcaaacg gtatttggca ttatttagtt aaaaaatgta gaaggagagt gaaacccatg 240

<210> 70
<211> 5
<212> PRT
<213> Listeria monocytogenes

<400> 70

Thr Glu Ala Lys Asp
1 5

<210> 71
<211> 5
<212> PRT
<213> Listeria monocytogenes

<400> 71

Asp Lys Ala Leu Thr
1 5

<210> 72
<211> 5
<212> PRT
<213> Bacillus subtilis

<400> 72

Val Gly Ala Phe Gly
1 5